

SEQUENCE LISTING

<110> E.I. du Pont de Nemours and Company

<120> Wuschel (WUS) Gene Homologs

<130> BB1410 PCT

<140>

<141>

<150> 60/157216

<151> 1999-10-01

<160> 25

<170> Microsoft Office 97

<210> 1

<211> 462

<212> DNA

<213> Zea mays

<400> 1

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ctgcaaaacta caggggtgtag tgatcgctga tcggctacat atcatatacc atggaggcgc 240
tgagcgggcg ggtaggcgtc aagtgcgggc ggtggaaccc tacggcggag caggtgaagg 300
tcctgacgga gctcttcgcg gcggggctgc ggacgcccag cacggagcag attcagcgca 360
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<210> 2

<211> 77

<212> PRT

<213> Zea mays

<400> 2

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Pro Thr Ala Glu Gln Val Lys Val Leu Thr Glu Leu Phe Arg Ala Gly
      20              25              30
```

```
Leu Arg Thr Pro Ser Thr Glu Gln Ile Gln Arg Ile Ser Asn Gln Leu
    35              40              45
```

```
Ser Ala Phe Gly Lys Gly Glu Asn Lys Asn Val Leu Leu Thr Gly Pro
    50              55              60
```

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Lys Gln Lys Gly Arg Glu Arg Gln Gln Gln Lys Lys Arg
    65              70              75
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<210> 3

<211> 1338

<212> DNA

<213> Zea mays

<400> 3

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aaccacacat	atagctgaag	caaataatc	cacttgctta	actggcggtg	tagtgtagct	180
gcgatcgctg	caaaactacag	ggtgtagtga	tcgtcgatcg	gctacatatc	atataccatg	240
gagggcgctga	gcgggcgggt	aggcgtaag	tcggggcggt	ggaaccctac	ggcggagcag	300
gtgaaggtcc	tgacggagct	cttccgcgcg	gggctgcgga	cgcccagcac	ggagcagatc	360
cagcgcacat	ccacccacct	cagcgccttc	ggcaaggtgg	agagcaagaa	cgtcttctac	420
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tcgtcgtcct	cccccgacag	cggcagcggc	aggggaagca	acaacgagga	agacggccgt	540
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ccggatgcgc	tgcgtgccac	tttttttttc	gttcatttat	gctggtctgt	gccctcatgc	1260
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aaaaaaaaaa	aaaaaaaaaa					1338

<210> 4
 <211> 220
 <212> PRT
 <213> Zea mays

<400> 4

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			20					25					30		
Leu	Arg	Thr	Pro	Ser	Thr	Glu	Gln	Ile	Gln	Arg	Ile	Ser	Thr	His	Leu
		35					40					45			
Ser	Ala	Phe	Gly	Lys	Val	Glu	Ser	Lys	Asn	Val	Phe	Tyr	Trp	Phe	Gln
	50					55				60					
Asn	His	Lys	Ala	Arg	Glu	Arg	His	His	His	Lys	Lys	Arg	Arg	Arg	Gly
65					70					75					80
Ala	Ser	Ser	Ser	Ser	Pro	Asp	Ser	Gly	Ser	Gly	Arg	Gly	Ser	Asn	Asn
				85				90						95	
Glu	Glu	Asp	Gly	Arg	Gly	Ala	Ala	Ser	Gln	Ser	His	Asp	Ala	Asp	Ala
			100					105					110		
Asp	Ala	Asp	Leu	Val	Leu	Gln	Pro	Pro	Glu	Ser	Lys	Arg	Glu	Ala	Arg
		115					120					125			
Ser	Tyr	Gly	His	His	His	Arg	Leu	Val	Thr	Cys	Tyr	Val	Arg	Asp	Val
	130					135					140				

Val Glu Gln Gln Glu Ala Ser Pro Ser Trp Glu Arg Pro Thr Arg Glu
145 150 155 160

Val Glu Thr Leu Glu Leu Phe Pro Leu Lys Ser Tyr Gly Asp Leu Glu
165 170 175

Ala Ala Glu Lys Val Arg Ser Tyr Val Arg Gly Ile Ala Ala Thr Ser
180 185 190

Glu Gln Cys Arg Glu Leu Ser Phe Phe Asp Val Ser Ala Gly Arg Asp
195 200 205

Pro Pro Leu Glu Leu Arg Leu Cys Ser Phe Gly Pro
210 215 220

<210> 5
<211> 720
<212> DNA
<213> Zea mays

<400> 5
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gtgcccgcgg ccggcgcggc ggacgccacc accagccaac tcggcgctcct ctgctgtcg 360
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aatggcgggc gatcggtgt gctgctggac acgagttccg actggggcag cagcggcgct 480
gccatggcca ccgagacatg cttcctgcag gtcggtgctg tagtacgttc ttttcttggg 540
cattgcgcgc agtttcacgt tcgtacgtac gagttgatcg ccgcgtcgtt ccatccaccg 600
gtatatataa ctgttaggta cggcgggtgcg cgcccgcagg actacatggg cgtgacggac 660
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<210> 6
<211> 238
<212> PRT
<213> Zea mays

<400> 6
Met Ala Ala Asn Ala Gly Gly Gly Gly Ala Gly Gly Gly Ser Gly Ser
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Gly Ser Val Ala Ala Pro Ala Val Cys Arg Pro Ser Gly Ser Arg Trp
20 25 30
Thr Pro Thr Pro Glu Gln Ile Arg Met Leu Lys Glu Leu Tyr Tyr Gly
35 40 45
Cys Gly Ile Arg Ser Pro Ser Ser Glu Gln Ile Gln Arg Ile Thr Ala
50 55 60
Met Leu Arg Gln His Gly Lys Ile Glu Gly Lys Asn Val Phe Tyr Trp
65 70 75 80
Phe Gln Asn His Lys Ala Arg Glu Arg Gln Lys Arg Arg Leu Thr Ser
85 90 95

Leu Asp Val Asn Val Pro Ala Ala Gly Ala Ala Asp Ala Thr Thr Ser
 100 105 110
 Gln Leu Gly Val Leu Ser Leu Ser Ser Pro Pro Pro Ser Gly Ala Ala
 115 120 125
 Pro Pro Ser Pro Thr Leu Gly Leu Tyr Ala Ala Gly Asn Gly Gly Gly
 130 135 140
 Ser Ala Val Leu Leu Asp Thr Ser Ser Asp Trp Gly Ser Ser Gly Ala
 145 150 155 160
 Ala Met Ala Thr Glu Thr Cys Phe Leu Gln Val Gly Ala Val Val Arg
 165 170 175
 Ser Phe Leu Gly His Cys Ala Gln Phe His Val Arg Thr Tyr Glu Leu
 180 185 190
 Ile Ala Ala Ser Phe His Pro Pro Val Tyr Ile Thr Val Arg Tyr Gly
 195 200 205
 Gly Ala Arg Pro Gln Asp Tyr Met Gly Val Thr Asp Thr Gly Ser Ser
 210 215 220
 Ser Gln Trp Pro Arg Phe Ser Ser Ser Asp Thr Ile Met Ala
 225 230 235

<210> 7
 <211> 767
 <212> DNA
 <213> Zea mays

<400> 7
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 ggcggtgtgc cgcccagcg gctcgcggtg gacgccgacg ccggagcaga tcaggatgct 180
 gaaggagctc tactacggct gcggcatccg gtcgcccagc tcggagcaga tccagcgcct 240
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 gccgccttca ggcgcggcgc ctccctcgcc caccctcggc ttctacgcg ccggcaatgg 480
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 ggccaccgag acatgcttcc tgcaggctcg tgctgtagta cgttcttttc ttgggcattg 600
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 tataactgtt aggtacggcg gtgcgcgccc gcaggactac atgggcgtga cggacacggg 720
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<210> 8
 <211> 237
 <212> PRT
 <213> Zea mays

<400> 8
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 20 25 30

Thr Pro Thr Pro Glu Gln Ile Arg Met Leu Lys Glu Leu Tyr Tyr Gly
 35 40 45
 Cys Gly Ile Arg Ser Pro Ser Ser Glu Gln Ile Gln Arg Ile Thr Ala
 50 55 60
 Met Leu Arg Gln His Gly Lys Ile Glu Gly Lys Asn Val Phe Tyr Trp
 65 70 75 80
 Phe Gln Asn His Lys Ala Arg Glu Arg Gln Lys Arg Arg Leu Thr Ser
 85 90 95
 Leu Asp Val Asn Val Pro Ala Ala Gly Ala Ala Asp Ala Thr Thr Ser
 100 105 110
 Gln Leu Gly Val Leu Ser Leu Ser Ser Pro Pro Pro Ser Gly Ala Ala
 115 120 125
 Pro Pro Ser Pro Thr Leu Gly Phe Tyr Ala Ala Gly Asn Gly Gly Gly
 130 135 140
 Ser Ala Val Leu Leu Asp Thr Ser Ser Asp Trp Gly Ser Ser Gly Ala
 145 150 155 160
 Ala Met Ala Thr Glu Thr Cys Phe Leu Gln Val Gly Ala Val Val Arg
 165 170 175
 Ser Phe Leu Gly His Cys Ala Gln Phe His Val Arg Thr Tyr Glu Leu
 180 185 190
 Ile Ala Ala Ser Phe His Pro Pro Val Tyr Ile Thr Val Arg Tyr Gly
 195 200 205
 Gly Ala Arg Pro Gln Asp Tyr Met Gly Val Thr Asp Thr Gly Ser Ser
 210 215 220
 Ser Gln Trp Pro Arg Phe Ala Ser Ser Asp Thr Ile Met
 225 230 235

<210> 9
 <211> 1367
 <212> DNA
 <213> Zea mays

<400> 9
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 cccgctattc ccagccttca gtagcagcag cagtacgtcg cgccctgccc atcgatccat 180
 ctggctatca tacctgtcga catggaaggc ggactgagcc cggagcggca cgcggcggcg 240
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 ttcaacagcg gcatggtgaa cccgccccaa gacgagacgg tccgcatccg caagctgctg 360
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 tcgtgcgagg ggatgatggg cgacctggac tacggcggcg gcgacgacct gttcgccatc 660
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cacacaaaca aatagagtgt tgtacctacg acgcatccac atcgaacatc tatactaagt 1320
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<210> 10
 <211> 253
 <212> PRT
 <213> Zea mays

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<400> 10
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  1              5              10              15

Arg Ser Arg Trp Thr Pro Lys Pro Glu Gln Ile Leu Ile Leu Glu Ser
      20              25              30

Ile Phe Asn Ser Gly Met Val Asn Pro Pro Lys Asp Glu Thr Val Arg
      35              40              45

Ile Arg Lys Leu Leu Glu Arg Phe Gly Ala Val Gly Asp Ala Asn Val
      50              55              60

Phe Tyr Trp Phe Gln Asn Arg Arg Ser Arg Ser Arg Arg Arg Gln Arg
      65              70              75              80

Gln Leu Gln Ala Gln Ala Ala Ala Ser Ser Ser Ser Ser Gly Ser Pro
      85              90              95

Pro Thr Ser Gly Leu Ala Pro Gly His Ala Thr Ala Ser Ser Thr Ala
      100             105             110

Gly Met Phe Ala His Gly Ala Thr Tyr Gly Ser Ser Ala Ser Ala Ser
      115             120             125

Trp Pro Pro Pro Pro Ser Cys Glu Gly Met Met Gly Asp Leu Asp Tyr
      130             135             140

Gly Gly Gly Asp Asp Leu Phe Ala Ile Ser Arg Gln Met Gly Tyr Ala
      145             150             155             160

Ser Gly Gly Gly Ser Gly Ser Ala Ser Ser Ala Ala Val Ala His His
      165             170             175

Glu Gln Gln Gln Gln Leu Tyr Tyr Ser Pro Cys Gln Pro Ala Ser Met
      180             185             190

Thr Val Phe Ile Asn Gly Val Ala Thr Glu Val Pro Arg Gly Pro Ile
      195             200             205

Asp Leu Arg Ser Met Phe Gly Gln Asp Val Met Leu Val His Ser Thr
      210             215             220

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<220>
 <221> unsure
 <222> (497)

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 cngggggngc gcgtttttat cttacangaa acccattcta ctttgctgcc ccgcaagggc 420
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<210> 12
 <211> 89
 <212> PRT
 <213> Zea mays

<220>
 <221> UNSURE
 <222> (53)

<220>
 <221> UNSURE
 <222> (55)

<400> 12
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 Ser Ala Glu Gln Ile Gln Gln Ile Thr Gly Arg Leu Arg Glu His Gly
 20 25 30
 Ala Ile Glu Gly Lys Asn Val Phe Tyr Trp Phe Gln Asn His Lys Ala
 35 40 45
 Arg Gln Arg Gln Xaa Gln Xaa Ala Gly Gln Leu Arg Leu Leu Gln Gln
 50 55 60
 Ala Pro Pro Pro Ala Pro Ala Ala Ala Arg Ala Leu His Ala Pro Arg
 65 70 75 80
 Ala Thr Val Pro Ser Arg Pro Arg Pro
 85

<210> 13
 <211> 1194
 <212> DNA
 <213> Zea mays

<400> 13
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 cgagcacggc ctgcgcaccc ccagcgcgga gcagatacag cagatcacgg gcaggctgcg 120
 ggagcacggc gccatcgagg gcaagaacgt cttctactgg ttccagaacc acaaggcccc 180
 ccagcgccag aggcagaagc aggacagctt cgcctacttc agcagggtcc tccgccggcc 240
 cccgccgctg cccgtgctct ccatgcccc cgcgccaccg taccatcacg cccgcgtccc 300


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ggcgccgccc gcgataccga tgcgatggc gccgcccgcg cccgctgcat gcaacgacaa 360
cggcggcgcg cgtgtgatct acaggaaccc attctacgtg gctgcgccgc aggcgcccc 420
tgcaaatgcc gcctactact acccacagcc acagcagcag cagcagcagc aggtgacagt 480
catgtaccag tacccgagaa tggaggtagc cggccaggac aagatgatga ccagggccgc 540
ggcgccaccg cagcagcagc acaacggcgc cgggcaacaa ccgggacgcg ccggccaccc 600
cagccgcgag acgctccagc tgttcccgcg tccagcccac cttcgtgctg cggcacgaca 660
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aaaaaaaaaa aaaaaaaaaa aaaaaaaaaa aaaaaaaaaa aaaaaaaaaa aaag 1194

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<210> 14

<211> 221

<212> PRT

<213> Zea mays

<400> 14

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20 25 30

Leu Arg Glu His Gly Ala Ile Glu Gly Lys Asn Val Phe Tyr Trp Phe
35 40 45

Gln Asn His Lys Ala Arg Gln Arg Gln Arg Gln Lys Gln Asp Ser Phe
50 55 60

Ala Tyr Phe Ser Arg Leu Leu Arg Arg Pro Pro Pro Leu Pro Val Leu
65 70 75 80

Ser Met Pro Pro Ala Pro Pro Tyr His His Ala Arg Val Pro Ala Pro
85 90 95

Pro Ala Ile Pro Met Pro Met Ala Pro Pro Pro Pro Ala Ala Cys Asn
100 105 110

Asp Asn Gly Gly Ala Arg Val Ile Tyr Arg Asn Pro Phe Tyr Val Ala
115 120 125

Ala Pro Gln Ala Pro Pro Ala Asn Ala Ala Tyr Tyr Tyr Pro Gln Pro
130 135 140

Gln Gln Gln Gln Gln Gln Gln Val Thr Val Met Tyr Gln Tyr Pro Arg
145 150 155 160

Met Glu Val Ala Gly Gln Asp Lys Met Met Thr Arg Ala Ala Ala His
165 170 175

Gln Gln Gln Gln His Asn Gly Ala Gly Gln Gln Pro Gly Arg Ala Gly
180 185 190

His Pro Ser Arg Glu Thr Leu Gln Leu Phe Pro Pro Pro Ala His Leu
 195 200 205

Arg Ala Ala Ala Arg Gln Gly Ala Arg Arg Gln Arg Gln
 210 215 220

<210> 15
 <211> 506
 <212> DNA
 <213> Glycine max

<220>
 <221> unsure
 <222> (19)

<220>
 <221> unsure
 <222> (489)..(490)

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 tagacatggt ggagaacttt tacaagcagg gaataaggac tcccagcact gagcaaatac 180
 aacagattac ctctaggctt agggcttatg gttacatcga gggaaaaaat gtcttctact 240
 ggtttcaaaa tcacaaagcg cgccaaagac agaagctcaa gcagaagcaa caaagcattg 300
 catactgcaa ttgcttttctt catgcctccc accccatttg ccaaaatgtt gtctgcgtcc 360
 atattgtttg caaaagagtg gattcagctt ttatcctcac caaccaaagg tgcttgcaag 420
 tgtaggatt agctcaaggg attgagactg ggtcctttgg catgctaaag aatatgtgat 480
 ggcatgcann agtgaacacc cggatt 506

<210> 16
 <211> 134
 <212> PRT
 <213> Glycine max

<400> 16
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 Gln Ile Asp Met Leu Glu Asn Phe Tyr Lys Gln Gly Ile Arg Thr Pro
 35 40 45
 Ser Thr Glu Gln Ile Gln Gln Ile Thr Ser Arg Leu Arg Ala Tyr Gly
 50 55 60
 Tyr Ile Glu Gly Lys Asn Val Phe Tyr Trp Phe Gln Asn His Lys Ala
 65 70 75 80
 Arg Gln Arg Gln Lys Leu Lys Gln Lys Gln Gln Ser Ile Ala Tyr Cys
 85 90 95
 Asn Cys Phe Leu His Ala Ser His Pro Ile Cys Gln Asn Val Val Cys
 100 105 110

Val His Ile Val Cys Lys Arg Val Asp Ser Ala Phe Ile Leu Thr Asn
 115 120 125

Gln Arg Cys Leu Gln Val
 130

<210> 17
 <211> 844
 <212> DNA
 <213> Glycine max

<400> 17
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 caagcaggga ataaggactc ccagcactga gcaaatacaa cagattacct ctaggcttag 180
 ggcttatggt tacatcgagg gaaaaaatgt cttctactgg tttcaaaatc acaaagcgcg 240
 ccaaagacag aagctcaagc agaagcaaca aagcattgca tactgcaatt gctttcttca 300
 tgctcccac cccatttgcc aaaatgttgt ctgcgctcca tattgtttgc aaaagagtgg 360
 attcagcttt tatcctcacc aaccaaaagt gtaggtatta gctcaaggat 420
 tgagactggg tcctttggca tgctaagaat atgtgatggc atgcagagtg aacaccgga 480
 ttataactat agcaccagta accgtgaagc cttaactcta tttcctcttc atccaaccgg 540
 tattttggaa gaaaaaacia ctcactcctc tgttgatgtc accgacaaat cttttgtttc 600
 tattgctggt gacgaaaatg gtcactcttg aaatcaaccc tgctttaatt ttcagtactg 660
 aagaacgaag gtatcgagat agtgattaag tatcatcgac caaaactact aacactgtac 720
 tactactttc tttagtagc tcgttggttca tcttcgaaat gagttttatc taattggata 780
 ttgagtttaa cgtagtaaaa aaaaaaaaaa aaaaaaaaaa aaaaaaaaaa aaaaaaaaaa 840
 aaaa 844

<210> 18
 <211> 217
 <212> PRT
 <213> Glycine max

<400> 18
 Ser His Ser Thr Ala Glu Asp Glu Ser Gly Trp Lys Gly Ser Ser Gly
 1 5 10 15
 Ala His Ser Ser Val Ser Arg Trp Ser Pro Thr Lys Glu Gln Ile Asp
 20 25 30
 Met Leu Glu Asn Phe Tyr Lys Gln Gly Ile Arg Thr Pro Ser Thr Glu
 35 40 45
 Gln Ile Gln Gln Ile Thr Ser Arg Leu Arg Ala Tyr Gly Tyr Ile Glu
 50 55 60
 Gly Lys Asn Val Phe Tyr Trp Phe Gln Asn His Lys Ala Arg Gln Arg
 65 70 75 80
 Gln Lys Leu Lys Gln Lys Gln Gln Ser Ile Ala Tyr Cys Asn Cys Phe
 85 90 95
 Leu His Ala Ser His Pro Ile Cys Gln Asn Val Val Cys Ala Pro Tyr
 100 105 110
 Cys Leu Gln Lys Ser Gly Phe Ser Phe Tyr Pro His Gln Pro Lys Val
 115 120 125

Leu Ala Ser Val Gly Ile Ser Ser Arg Ile Glu Thr Gly Ser Phe Gly
 130 135 140
 Met Leu Arg Ile Cys Asp Gly Met Gln Ser Glu His Pro Asp Tyr Asn
 145 150 155 160
 Tyr Ser Thr Ser Asn Arg Glu Ala Leu Thr Leu Phe Pro Leu His Pro
 165 170 175
 Thr Gly Ile Leu Glu Glu Lys Thr Thr His His Ser Val Asp Val Thr
 180 185 190
 Asp Lys Ser Phe Val Ser Ile Ala Val Asp Glu Asn Gly His Leu Gly
 195 200 205
 Asn Gln Pro Cys Phe Asn Phe Gln Tyr
 210 215

<210> 19
 <211> 741
 <212> DNA
 <213> Glycine max

<400> 19
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 atgtaaggac tcattcatca gtttcacggt ggagtcctac aaaggagcaa atagacatgt 120
 tagagaacct ttacaagcag ggaataagga ctcccagcac tgagcaaata caacagatta 180
 cctctaggct cagggttat ggtcacatcg agggaaagaa tgtcttctac tgggtttcaaa 240
 atcacaaagc tcgtcaaaga cagaagctga tgaagcaaca aaccattgca tattccaatc 300
 gctttcttcg tgccctccac cccatttgcc aaaatgttgc ctgcgctcca tattgtttgc 360
 aacggagtgg attcagcttt tatcctcaac aatcgaaggt gcttgcaagt ggaggtataa 420
 gttcaactgg gccttttaggc atgcaaagaa tgtttgatgg catgcagagt agtgaacacc 480
 cggattgtaa ccgtgaagtc ttaactctct ttccctcttca tccaaccggc attttgaaag 540
 aaaaaacaac tcatcaagt ccttcccttg cttcaacttc tgttggtgct gttgatgaag 600
 atggtcatct tggaaatcag cccttcttta attttttcac tactgaacca aggtcgagag 660
 agtgattagg tgtaattgt cattgaccaa aaaaacaact aacatggcac tactttgagt 720
 aaaaaaaaa aaaaaaaaa a 741

<210> 20
 <211> 212
 <212> PRT
 <213> Glycine max

<400> 20
 Met Glu Ser His Ser Ser Asp Ala Glu Ala Glu Asn Val Arg Thr His
 1 5 10 15
 Ser Ser Val Ser Arg Trp Ser Pro Thr Lys Glu Gln Ile Asp Met Leu
 20 25 30
 Glu Asn Leu Tyr Lys Gln Gly Ile Arg Thr Pro Ser Thr Glu Gln Ile
 35 40 45
 Gln Gln Ile Thr Ser Arg Leu Arg Ala Tyr Gly His Ile Glu Gly Lys
 50 55 60
 Asn Val Phe Tyr Trp Phe Gln Asn His Lys Ala Arg Gln Arg Gln Lys
 65 70 75 80

<400> 22

Met Lys Val His Gln Phe Ala Arg Gly Phe Trp Glu His Glu Pro Ser
1 5 10 15

Leu Thr Leu Gly Cys Lys Arg Leu Arg Pro Leu Ala Pro Lys Leu Ser
20 25 30

Asn Thr Asp Thr Ile Ser Pro Pro His His Pro Val Thr Thr Phe Asp
35 40 45

Leu Lys Ser Phe Ile Lys Pro Glu Ser Ala Ser Arg Lys Leu Gly Ile
50 55 60

Gly Ser Ser Asp Asp Asn Thr Asn Lys Arg Asp Pro Ser Ser Pro Gln
65 70 75 80

Gly Gln Ala Glu Thr His Ile Pro Gly Gly Thr Arg Trp Asn Pro Thr
85 90 95

Gln Glu Gln Ile Gly Ile Leu Glu Met Leu Tyr Arg Gly Gly Met Arg
100 105 110

Thr Pro Asn Ala Gln Gln Ile Glu Gln Ile Thr Ala Gln Leu Ser Lys
115 120 125

Tyr Gly Lys Ile Glu Gly Lys Asn Val Phe Tyr Trp Phe Gln Asn His
130 135 140

Lys Ala Arg Glu Arg Gln Lys Gln Lys Arg Asn Asn Leu Gly Leu Ala
145 150 155 160

His Ser Pro Arg Thr Thr Leu Thr Thr Ser Pro Pro Phe Ser Cys Cys
165 170 175

Val Ile Thr Thr Met Asp Thr Thr Lys Arg Gly Glu Val Val Glu Arg
180 185 190

Glu Glu Glu Asp Ser Pro Leu Lys Lys Cys Arg Ser Trp Ala Phe Glu
195 200 205

Tyr Leu Glu Asp Gln Arg Glu Glu Glu His Arg Thr Leu Glu Leu Phe
210 215 220

Pro Leu His Pro Glu Gly Arg
225 230

<210> 23

<211> 904

<212> DNA

<213> Glycine max

<400> 23

cagcatgaag gtgcatcagt tcacacgtgg attaatctgg gagcacgaac ctttcctcac 60
acttggctgc aagagattac gccctcttgc tcccaagctt cccaacacca aaactatcac 120
taccctttc gatctcaaga gcttcatcag gcccgaaggt ggcccagaa aaccggtttc 180
ctctgacgac actaagaagg atccaccttc accccaaggt cagattgaaa cgcaccagg 240
agggacacgg tggaatccta cgcaagaaca gataggcata ttggagatgt tgtacaaagg 300
agggatgcga actccgaatg ctcaacagat agagcagatc actgtccagc ttggaaagta 360
cggcaagatc gaagggaaga acgtgttcta ttggtttcag aatcacaaag cacgcgagag 420

acaaaagcag aagcgcagca gccttgcac ttctcatagt cctcgaactc ccacaattca 480
 cagtgttgtt actttggaga caacaagggg ggaagtggta gagagagatc acgaggaaga 540
 tagtccgtac aagaagaagt gcaggagatg ggtatttgac tgcttggaag aacaaaacat 600
 gtcacacact tgtgaacaag aggaacatag aactctggag ctttttccat tgcacccgga 660
 aggcagatga aggggtttga gtttgattga ccatttatct atcatttttc actttgcttt 720
 agttccgaat cgcagctgat tattgaatga atgtgggtta attaatttgc tttacttttc 780
 ttttttcttt gtattgggaa agaagaaaga caaagttgtc tctgatctgt actcttcac 840
 ttaatgctat tcctgacttt ggaacaaaaa aaaaaaaaaa aaaactcgga gagagcgaac 900
 tagt 904

<210> 24
 <211> 221
 <212> PRT
 <213> Glycine max

<400> 24

Met Lys Val His Gln Phe Thr Arg Gly Leu Ile Trp Glu His Glu Pro
 1 5 10 15
 Phe Leu Thr Leu Gly Cys Lys Arg Leu Arg Pro Leu Ala Pro Lys Leu
 20 25 30
 Pro Asn Thr Lys Thr Ile Thr Thr Pro Phe Asp Leu Lys Ser Phe Ile
 35 40 45
 Arg Pro Glu Ser Gly Pro Arg Lys Pro Val Ser Ser Asp Asp Thr Lys
 50 55 60
 Lys Asp Pro Pro Ser Pro Gln Gly Gln Ile Glu Thr His Pro Gly Gly
 65 70 75 80
 Thr Arg Trp Asn Pro Thr Gln Glu Gln Ile Gly Ile Leu Glu Met Leu
 85 90 95
 Tyr Lys Gly Gly Met Arg Thr Pro Asn Ala Gln Gln Ile Glu Gln Ile
 100 105 110
 Thr Val Gln Leu Gly Lys Tyr Gly Lys Ile Glu Gly Lys Asn Val Phe
 115 120 125
 Tyr Trp Phe Gln Asn His Lys Ala Arg Glu Arg Gln Lys Gln Lys Arg
 130 135 140
 Ser Ser Leu Ala Ser Ser His Ser Pro Arg Thr Pro Thr Ile His Ser
 145 150 155 160
 Val Val Thr Leu Glu Thr Thr Arg Gly Glu Val Val Glu Arg Asp His
 165 170 175
 Glu Glu Asp Ser Pro Tyr Lys Lys Lys Cys Arg Arg Trp Val Phe Asp
 180 185 190
 Cys Leu Glu Glu Gln Asn Met Ser Ser Pro Cys Glu Gln Glu Glu His
 195 200 205
 Arg Thr Leu Glu Leu Phe Pro Leu His Pro Glu Gly Arg
 210 215 220

<210> 25
 <211> 291
 <212> PRT
 <213> Arabidopsis thaliana

<400> 25

Met	Glu	Pro	Pro	Gln	His	Gln	His	His	His	His	Gln	Ala	Asp	Gln	Glu	1	5	10	15
Ser	Gly	Asn	Asn	Asn	Asn	Lys	Ser	Gly	Ser	Gly	Gly	Tyr	Thr	Cys	Arg	20	25	30	
Gln	Thr	Ser	Thr	Arg	Trp	Thr	Pro	Thr	Thr	Glu	Gln	Ile	Lys	Ile	Leu	35	40	45	
Lys	Glu	Leu	Tyr	Tyr	Asn	Asn	Ala	Ile	Arg	Ser	Pro	Thr	Ala	Asp	Gln	50	55	60	
Ile	Gln	Lys	Ile	Thr	Ala	Arg	Leu	Arg	Gln	Phe	Gly	Lys	Ile	Glu	Gly	65	70	75	80
Lys	Asn	Val	Phe	Tyr	Trp	Phe	Gln	Asn	His	Lys	Ala	Arg	Glu	Arg	Gln	85	90	95	
Lys	Lys	Arg	Phe	Asn	Gly	Thr	Asn	Met	Thr	Thr	Pro	Ser	Ser	Ser	Pro	100	105	110	
Asn	Ser	Val	Met	Met	Ala	Ala	Asn	Asp	His	Tyr	His	Pro	Leu	Leu	His	115	120	125	
His	His	His	Gly	Val	Pro	Met	Gln	Arg	Pro	Ala	Asn	Ser	Val	Asn	Val	130	135	140	
Lys	Leu	Asn	Gln	Asp	His	His	Leu	Tyr	His	His	Asn	Lys	Pro	Tyr	Pro	145	150	155	160
Ser	Phe	Asn	Asn	Gly	Asn	Leu	Asn	His	Ala	Ser	Ser	Gly	Thr	Glu	Cys	165	170	175	
Gly	Val	Val	Asn	Ala	Ser	Asn	Gly	Tyr	Met	Ser	Ser	His	Val	Tyr	Gly	180	185	190	
Ser	Met	Glu	Gln	Asp	Cys	Ser	Met	Asn	Tyr	Asn	Asn	Val	Gly	Gly	Gly	195	200	205	
Trp	Ala	Asn	Met	Asp	His	His	Tyr	Ser	Ser	Ala	Pro	Tyr	Asn	Phe	Phe	210	215	220	
Asp	Arg	Ala	Lys	Pro	Leu	Phe	Gly	Leu	Glu	Gly	His	Gln	Asp	Glu	Glu	225	230	235	240
Glu	Cys	Gly	Gly	Asp	Ala	Tyr	Leu	Glu	His	Arg	Arg	Thr	Leu	Pro	Leu	245	250	255	
Phe	Pro	Met	His	Gly	Glu	Asp	His	Ile	Asn	Gly	Gly	Ser	Gly	Ala	Ile	260	265	270	
Trp	Lys	Tyr	Gly	Gln	Ser	Glu	Val	Arg	Pro	Cys	Ala	Ser	Leu	Glu	Leu	275	280	285	

Arg Leu Asn
290